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(54) Title: DNA ENCODING 2-ACYLTRANSFERASES

(57) Abstract

Plants, particularly transgenic plants, may be produced having a 2-acyltransferase enzyme or other insoluble acyltransferase enzyme with an altered substrate specificity compared to the native enzyme. For example, oil seed rape (*Brassica napus*) may contain a 2-acyltransferase transgene derived from *Limnanthes douglassi* in order to increase the erucic acid content of the oil. The cDNA sequence of maize (*Zea mays*) 2-acyltransferase is disclosed and is useful for cloning acyltransferase genes and/or cDNAs from other organisms, including *L. douglassi*.

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DNA ENCODING 2-ACYLTRANSFERASES

This invention relates to modified plants. In particular, the invention relates to plants modified such 5 that at least part of the plant (for example seeds of the plant) is capable of yielding a commercially useful oil.

Plants have long been a commercially valuable source of oil. Nutritional uses of plant-derived oils have 10 hitherto been dominant, but attention is now turning additionally to plants as a source of industrially useful oils, for example as replacements for or improvements on mineral oils. Oil seeds, such as from rape, have a variety of lipids in them (Hildish & Williams, "Chemical 15 Composition of Natural Lipids", Chapman Hall, London, 1964). There is now considerable interest in altering lipid composition by the use of recombinant DNA technology (Knauf, TIBtech, February 1987, 40-47), but by no means all of the goals have been realised to date for 20 a variety of reasons, in spite of the ever-increasing sophistication of the technology.

Success in tailoring the lipid content of plant-derived 25 oils requires a firm understanding of the biochemistry and genes involved. Broadly, two approaches are available. First, plants may be modified to permit the synthesis of fatty acids which are new (for the plant); so, for example, laurate and/or stearate may be synthesised in rape. Secondly, the pattern and/or extent 30 of incorporation of fatty acids into the glycerol backbone of the lipid may be altered. It is with this latter approach that the present invention is concerned, although the former approach may additionally be used.

Lipids are formed in plants by the addition of fatty acid moieties onto the glycerol backbone by a series of acyl transferase enzymes. There are three positions on the glycerol molecule at which fatty acid (acyl) moieties may be substituted, and the substitution reached at each position is catalysed by a position-specific enzyme: the enzymes are known as 1-, 2- and 3-acyltransferases, respectively.

One, but not the only, current aim of "lipid engineering" in plants is to provide oils including lipids with a high content of erucic (22:1) acid. Erucic acid-containing lipids are commercially desirable for a number of purposes, particularly as replacements to or supplements for mineral oils in certain circumstances, as alluded to above. In the case of oil seed rape (*Brassica napus*), one of the most significant oil producing crops in cultivation today, the specificity of the 2-acyltransferase enzyme positively discriminates against the incorporation of erucic acid at position 2. So, even in those cultivars of rape which are able to incorporate erucic acid at positions 1 and 3, where there is no (or at least reduced) discrimination against erucic acid, only a maximum 66% of the fatty acids incorporated into triacyl glycerols can be erucic acid. Such varieties of rape are known as HEAR (high erucic acid rape) varieties.

It would therefore be desirable to increase the erucic acid content of conventional oil seed rape, as well as HEAR varieties; the same can be said of oils of other vegetable oil crops such as maize, sunflower and soya, to name but a few examples. While in principle it may be thought possible to introduce into a desired plant DNA encoding a 2-acyltransferase of different fatty acid

specificity, for example from a different plant, in practice there are a number of problems.

First, 2-acyltransferase and 3-acyltransferase are membrane bound, and therefore insoluble, enzymes. They have not been purified. This makes working with them difficult and rules out the use of many conventional DNA cloning procedures. This difficulty does not, paradoxically, lie in the way of cloning the gene (or at least cDNA) encoding the 1-acyltransferase enzyme, which is soluble: in fact, recombinant DNA work has already been undertaken on this enzyme for a completely different purpose, namely the enhancement of chilling resistance in tobacco plant leaves, by Murata et al (*Nature* 356 710-713 (1992)).

Secondly, very little is known about the 2- and 3- acyltransferases. There is no idea of their size or how they are targeted to membranes. No nucleotide or amino acid sequence data are available and no antibodies have been raised against them.

Although there has been discussion, therefore, of the desirability of modifying 2-acyltransferase specificity, for example by importing a gene coding for the corresponding enzyme, but of different specificity, from another species, there is a pressing need in the art for the key which enables this work to be done. The present invention provides such a key, in the form of a DNA sequence (in the specific case, a cDNA sequence) encoding a 2-acyltransferase. The DNA sequence in Figure 1 from nucleotides 130 to 1254 encodes the 2-acyltransferase from maize (*Zea mays*), including the stop codon.

According to a first aspect of the invention, therefore, there is provided a recombinant or isolated DNA sequence, preferably encoding an enzyme having membrane-bound acyltransferase activity, and selected from:

5

(i) a DNA sequence comprising the DNA sequence of Figure 1 encoding at least from MET₄₄ to Stop₄₁₈ (SEQ ID: 2) or its complementary strand,

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(ii) nucleic acid sequences hybridising to the DNA sequence of Figure 1 (SEQ ID: 1), or its complementary strand, under stringent conditions, and

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(iii) nucleic acid sequences which would hybridise to the DNA sequence of Figure 1 (SEQ ID: 1), or its complementary strand, but for the degeneracy of the genetic code.

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Fragments of the above DNA sequences, for example of at least 15, 20, 30, 40 or 60 nucleotides in length, are also within the scope of the invention.

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Suitable stringent conditions include salt solutions of approximately 0.9 molar at temperatures of from 35°C to 65°C. More particularly, stringent hybridisation conditions include 6 x SSC, 5 x Denhardt's solution, 0.5% SDS, 0.5% tetrasodium pyrophosphate and 50µg/ml denatured herring sperm DNA; washing may be for 2 x 30 minutes at 65°C in 1 x SSC, 0.1% SDS and 1 x 30 minutes in 0.2 x SSC, 0.1% SDS at 65°C.

Nucleic acid sequences within the scope of the first aspect of the invention will generally encode a protein

having 2-acyltransferase activity, as that is the activity of the enzyme encoded by the Figure 1 nucleic acid sequence. Nucleic acid sequences not encoding a protein having enzymic activity (or the relevant enzymic activity) but otherwise conforming to the first aspect of the invention as set out above may be useful for other purposes (and are therefore also encompassed by the invention); for example they may be useful as probes, which is a utility shared by the nucleic acid sequences of the first aspect of the invention, including the Figure 1 sequence itself.

The probe utility arises as follows. As there is likely to be a high degree of homology between acyltransferases of different species (and particularly between 2-acyltransferases of different species) the Figure 1 sequence (or part of it, or other sequences within the invention) may be used to probe cDNA or genomic libraries of other species in order to clone DNA sequences encoding acyltransferases having desired specificities. For example, if it is desired to produce oil having a high content of erucic acid esterified to glycerol, a DNA library of any species which naturally makes erucic acid may be probed. Suitable plants include meadow foam (*Limnanthes* spp., especially *L. alba* and, particularly, *L. douglassii*) and *Crambe*. *Limnanthes douglassii* is the preferred species, as specificity studies show that there is positive discrimination towards incorporation of erucic acid into position 2 of the triacylglyceride. Libraries of organisms other than the higher plants may be probed; for example, certain bacteria may have an acyltransferase of the desired specificity.

DNA in accordance with the invention will in general have a higher degree of homology with at least part of the Figure 1 sequence than with known sequences.

5 Recombinant DNA in accordance with the invention may be in the form of a vector, which may have sufficient regulatory sequences (such as a promoter) to direct expression. Vectors which are not expression vectors are useful for cloning purposes (as expression vectors themselves may be). Host cells (such as bacteria and 10 plant cells) containing vectors in accordance with the invention themselves form part of the invention.

15 DNA sequences in accordance with the invention can be used in another way in cloning a gene of interest from another species: if the DNA is coupled to a suitable promoter, for example on an expression vector in a suitable host organism, protein may be produced. Such 20 protein may be used to generate polyclonal or monoclonal antibodies, or other binding molecules, which may then be used to screen for expression of homologous proteins in other species, for example as part of a DNA library screening programme.

25 Suitable cDNA libraries of target species will generally be prepared when the gene of interest is likely to be expressed; so cDNA embryo libraries (prepared at the early lipid synthesis stage), for example of *Limnanthes* spp. will be preferred.

30 The invention therefore enables the cloning of a wide variety of genes (or, more generally, DNA sequences) encoding acyltransferases, and 2-acyltransferases in particular, using DNA sequences as described above.

Such acyltransferases, such as from *Limnanthes* spp. may also be cloned directly, for example using complementation studies, from a DNA library of the species in question. For example, if *E. coli* is used as the complementation host, a mutant is chosen which is defective in the relevant enzyme (for example 2-acyltransferase); the DNA library from the target species (such as *L. douglassi*) is cloned into the mutant complementation host; host cells incorporating the target acyltransferase gene in their genome can readily be selected using appropriate selective media. *E. coli* mutant JC201 is a suitable host for use in complementation studies relating to 2-acyltransferase.

Cloning the acyltransferase gene of choice into a microbial host, such as a bacterium like *E. coli*, in such a way that the gene can be expressed has a particularly advantage in that the substrate specificity of the acyltransferase gene can be assessed in the microbial host before transformed plants are prepared, thereby saving considerably on research time. Such an assessment may be made by competitive substrate assays, in which differently detectably labelled candidate substrates for the enzyme compete with each other for incorporation into the glyceride. For example, ^{14}C -erucyl CoA and ^3H -oleoyl CoA can be used as competitive substrates for 2-acyltransferase, and the relative amounts of ^{14}C or tritium uptake into glyceride can be measured. (As 2-acyltransferases have acceptor, glycerol-based, substrates and donor, fatty acid-based, substrates, the experiment can be carried out with different acceptors, such as 1-erucyl-glycerol-3-phosphate and 1-oleoyl-glycerol-3-phosphate.) A gene coding for an enzyme which preferentially donates erucic acid to the acceptor

(particularly 1-erucyl-glycerol-3-phosphate) may by this means be identified as a DNA sequence of choice for further use in the invention as described below.

5 In a second aspect of the invention, there is provided a plant having one or more insoluble acyltransferase enzymes having a substrate specificity which differs from the native enzyme of the plant.

10 While site-directed mutagenesis and/or other protein engineering techniques may be used to alter the specificity of an enzyme native to the plant, it is preferred that the plant be transgenic and incorporate an expressible acyltransferase gene encoding an enzyme of the desired specificity from another species. 2-acyltransferases are the enzymes of choice. For example, as described above, a 2-acyltransferase enzyme which has an enhanced specificity for, or at least no discrimination against, erucic acid, may be made by this means to express in a plant which would not normally incorporate erucic acid into triacylglycerides. An important embodiment of the invention relates to genetically engineered plants which have higher levels of erucic acid incorporated into triacylglycerols than in corresponding non-engineered plants. Preferable though this embodiment may be, though, the invention is not limited to the enhancement of erucic acid incorporation into glycerides: other acids may be desired in other circumstances.

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30 For the acyltransferase transgene to be expressible, a promoter has to be operatively coupled to it. Because at the present state of the art it is difficult precisely to regulate the site of incorporation of a transgene into

the host genome, it is preferred that the transgene be coupled to its promoter prior to transformation of the plant. Promoters useful in the invention may be temporal- and/or seed-specific, but there is no need for them to be so: constitutive promoters, such as the CaMV 5 35S promoter, may be in fact be preferred because they are usually strong promoters. Other tissues are unlikely to be adversely affected if the transgene encoding the acyltransferase enzyme is expressed in them, as the availability of the fatty acid CoA substrates is 10 effectively limited to the seed.

The promoter-transgene construct, once prepared, is introduced into plant cells by any suitable means. The 15 invention extends to such plant cells. Preferably, DNA is transformed into plant cells using a disarmed Ti-plasmid vector and carried by *Agrobacterium* by procedures known in the art, for example as described in EP-A-0116718 and EP-A-0270822. Alternatively, the foreign DNA 20 could be introduced directly into plant cells using an electrical discharge apparatus. This method is preferred where *Agrobacterium* is ineffective, for example where the recipient plant is monocotyledonous. Any other method that provides for the stable incorporation of the DNA 25 within the nuclear DNA of any plant cell of any species would also be suitable. This includes species of plant which are not currently capable of genetic transformation.

30 Preferably DNA in accordance with the invention also contains a second chimeric gene (a "marker" gene) that enables a transformed plant or tissue culture containing the foreign DNA to be easily distinguished from other plants or tissue culture that do not contain the foreign

DNA. Examples of such a marker gene include antibiotic resistance (Herrera-Estrella et al, *EMBO J.* 2(6) 987-95 (1983) and Herrera-Estrella et al, *Nature* 303 209-13 (1983)), herbicide resistance (EP-A-0242246) and glucuronidase (GUS) expression (EP-A-0344029). Expression of the marker gene is preferably controlled by a second promoter which allows expression in cells other than the tapetum, thus allowing selection of cells or tissue containing the marker at any stage of regeneration of the plant. The preferred second promoter is derived from the gene which encodes the 35S subunit of Cauliflower Mosaic Virus (CaMV) coat protein. However any other suitable second promoter could be used.

A whole plant can be regenerated from a single transformed plant cell, and the invention therefore provides transgenic plants (or parts of them, such as propagating material) including DNA in accordance with the invention as described above. The regeneration can proceed by known methods.

In one embodiment of the invention, the transgenic plant's native acyltransferase gene which corresponds to the transgene may be rendered at least partially inoperative or removed. So, if the transgene encodes a 2-acyltransferase, the plant's native 2-acyltransferase may be rendered inoperative by, for example, antisense or ribozyme techniques, as is known in the art.

By means of the invention, plants generating oil with a tailored lipid content may be produced. For example, the lipid composition of triacylglycerides in a plant may be substantially altered to produce triacylglycerides with a desired fatty acid (for example erucic acid) content

higher than has hitherto been possible. For example, oil seed rape (*B. napus*) may be transformed to produce oil whose triacylglyceride has an erucic acid content of over 70%.

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It can readily be seen that plants with increased lipid levels may be produced by means of the invention. However, the invention is also useful for producing plants with decreased lipid levels, which may be desired if elevated protein and/or starch levels are required. Decreased lipid levels may be achieved by interfering with the proper functioning of a gene encoding a 2-acyltransferase, for example by antisense or ribozyme technology. (Such reduced-lipid plants may if desired be further engineered for higher protein and/or starch content, if wished.)

Promoters which naturally drive 2-acyltransferases may also be obtained by hybridisation and/or restriction and/or sequencing studies using the Figure 1 sequence.

The invention enables the production of protein encoded by DNA of the first aspect of the invention, should that be desired. The protein may be expressed by host cells harbouring DNA in the form of an expression vector. The protein, which may be an enzyme having 2-acyltransferase activity, may have an amino acid sequence which is identical to or homologous with the Figure 1 sequence. The degree of homology will generally be greater than that of known proteins, and may be at least 40, 50, 60, 70, 80, 90, 95 or 99%.

Preferred features of each aspect of the invention are as for each other aspect *mutatis mutandis*.

The invention is illustrated by the following examples. The examples refer to the accompanying drawings, in which:

5 FIGURE 1 shows the cDNA sequence derived in Example 1 (SEQ ID: 1) and its derived protein sequence (SEQ ID: 2).

10 FIGURE 2 shows a sequence alignment of part of the gene products of *plsB* (SEQ ID: 3) and *plsC* (SEQ ID: 4) with part of the sequence shown in Figure 1 (SEQ ID: 5), showing a conserved motif. *plsB* is the *E. coli* *sn*-glycerol-3-phosphate acyltransferase gene and *plsC* the 1-acyl-*sn*-glycerol-3-phosphate acyltransferase gene of *E. coli*. Double points indicate exact matches between two sequences and a single point conservative amino acid substitutions. Stars indicate identical amino acids in all three sequences and residues conserved in two out of the three sequences are marked by a + symbol.

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FIGURES 3A, 3B and 3C: Membrane phospholipids from *E. coli* strains were extracted into chloroform and separated by 2-dimensional thin layer chromatography. The first dimension (ascending) was developed using chloroform:methanol:water (65:25:4) and the second dimension (left to right) developed with chloroform:methanol:acetic acid (65:25:10). Phospholipids were visualised by autoradiography for 16 hours at -70°C using Fuji RX film. The *E. coli* strains used were (Figure 3A): JC201 which carries a thermosensitive mutation in the 1-acyl-*sn*-glycerol-3-phosphate acyltransferase gene; (Figure 3B): JC201 containing the plasmid pPLSC, which

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encodes the *E. coli* 1-acyl-sn-glycerol-3-phosphate acyltransferase gene; (Figure 3C): JC201 containing the plasmid whose cDNA insert sequence is shown in Figure 1. LPA, lysophosphatidic acid; PE, phosphatidylethanolamine; CL, cardiolipin; PG, phosphatidylglycerol; PA, phosphatidic acid; O, origin. 20% of the ^{32}P is incorporated in LPA in JC201 and all of the corresponding label is incorporated in PE in both of the other two strains.

10

FIGURE 4: Acyltransferase assays were performed using ^{32}P -labelled lysophosphatidic acid which had been extracted from the *E. coli* strain JC201 and oleoyl CoA as an acyl donor. Phospholipids present in the reaction mixtures were extracted into chloroform and separated using silica gel thin layer chromatography. Chloroform:methanol:acetic acid:water (25:15:4:2) was used to develop the plates. The phospholipids were visualised by autoradiography for 16 hours at -70°C using Fuji RX film. The *E. coli* strains used were: JC201 which carries a thermosensitive mutation in the 1-acyl-sn-glycerol-3-phosphate acyltransferase gene; JC201 containing the plasmid pPLSC which encodes the *E. coli* 1-acyl-sn-glycerol-3-phosphate acyltransferase gene; JC201 containing the plasmid whose maize cDNA insert sequence is shown in Figure 1. LPA, lysophosphatidic acid; PA, phosphatidic acid.

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FIGURE 5 shows a comparison of the protein sequence shown in Figure 1 (SEQ ID: 6) with that derived (SEQ ID: 7) from a *B. napus* seed cDNA insert which was isolated by DNA hybridisation to the maize cDNA sequence. The sequences were aligned with the FastA

5 Maize = 374 aa vs. rape = 311 aa
51.5% identity; Optimised score: 705

EXAMPLE 1

Derivation of the Figure 1 cDNA sequence

10 Complementation studies using a maize cDNA expression library transferred into the *E. coli* mutant JC201 allowed the isolation of a plasmid encoding a 2-acyltransferase enzyme from maize. The cDNA insert of this plasmid is 1.6kb in size, and includes a poly A tail of 70bp. The 15 insert was sequenced to give the data shown and translation of the sequence revealed the present of only one large open reading frame. This is shown on Figure 1 with proposed start methionine and stop codon boxed. The 20 2-acyltransferase is 374 amino acids in size and sequencing upstream of open reading from showed that the protein is expressed as part of a fusion protein in *E. coli*. This consists of 10 amino acids of the β -galactosidase protein, 43 amino acids (shown in sequence) corresponding to the 5' untranslated region of the mRNA 25 and the 374 amino acid protein. Protein sequence comparisons of the large open reading frame with the 2-acyltransferase of *E. coli* show little overall identity but there is a stretch of 80 residues which has a high level of conservative substitution and contains some 30 amino acids that are conserved in the 2-acyltransferase, 1-acyltransferase and N-acetyl glucosamine acyltransferase of *E. coli*.

EXAMPLE 2**Incorporation of ^{32}P into total phospholipids**

E. coli strains were grown in minimal medium containing ^{32}P orthophosphate. Total glycerolipids were extracted into organic solvents and separated by 2D thin layer chromatography (Figure 3) (Lysophosphatidic acid (LPA) is the substrate for 2-acyltransferase (2-AT)).

As can be seen in Figure 3A, the accumulation of ^{32}P -labelled LPA in the mutant JC 201 illustrates the absence of a fully functional 2-AT. Addition of a plasmid carrying either the native *E. coli* gene (Figure 3B), or the maize clone given in Figure 1 (Figure 3C) restores 2-AT activity to the cells, allowing LPA to be removed and further metabolised. (Lysophosphatidic acid.)

These data indicate that the DNA sequence given in Figure 1 codes for 2-AT.

EXAMPLE 3**Over expression of the cDNA**

The cDNA region specifying the protein sequence given in Figure 1 was cloned into the *E. coli* overexpression vector pET11d (Studier et al, *Meth. Enzymol.* 185 60-89 (1990)). Increased 2-acyltransferase activity following induction of expression from the plasmid insert confirmed that the sequence in Figure 1 is that of 2-AT.

EXAMPLE 4**Localisation of 2-AT activity in *E. coli* cells containing the maize clone**

2-acyltransferase assays were carried out using membranes isolated from the mutant strain JC.201 which lacks 2-AT and from JC.201 containing the maize plasmid (Figure 4).

2-AT activity was not detected in membrane fractions from JC.201. The addition of a plasmid carrying the native *E. coli* gene or the sequence given in Figure 1, to JC.201 resulted in restoration of 2-AT activity to the membranes.

EXAMPLE 5

Using the maize cDNA as a heterologous probe to obtain cDNA from oilseed rape

A seed cDNA library from *Brassica napus* was screened with the sequence given in Figure 1, using standard techniques (Sambrook et al "Molecular Cloning - A Laboratory Manual", 2nd Edition, Cold Spring Harbor Laboratory Press, 1989).

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Conditions

For the hybridisation of the maize cDNA insert to the rape library: hybridisation was in 6xSSC, 5xDenhardts solution, 0.5% SDS, 0.5% tetradsodium pyrophosphate and 50ugml⁻¹ denatured herring sperm DNA. The filters were washed 2 x 30 minutes at 65°C in 1xSSC, 0.1%SDS and 1 x 30 minutes in 0.2xSSC, 0.1%SDS at 65°C.

A hybridising clone was sequenced and a protein sequence derived for the large ORF. Alignment of this protein sequence with that derived from the maize cDNA clone given in Figure 1, is shown in Figure 5.

The strong identity between these sequences illustrates the potential of using the sequence given in Figure 1 to obtain other 2-ATS.

EXAMPLE 6**Transgenic plants**

The sequence given in Figure 1 can be cloned, alongside a suitable promoter, into a suitable vector for expression in plants. The vector can be used to transform plants and the resulting plants expressing the 2-AT can be analysed for lipid content. Lipid metabolism is expected to be upregulated and elevated lipid levels were detectable in seeds.

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EXAMPLE 7**Antisense**

The sequence given in Figure 1 may be cloned, alongside a suitable promoter, in the antisense orientation into a suitable vector for expression in plants. The vector can be used to transform plants and the resulting plants expressing the 2-AT can be analysed for protein and starch content. Elevated levels of starch and protein are expected to be detectable in seeds.

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EXAMPLE 8**Down-regulation of Native 2-AT**

The DNA sequence of a 2-AT derived from *L. douglassii* (obtained as described in Example 5) can be introduced into oilseed rape (OSR) under the expression of a suitable promoter, using vectors and plant transformation methods well known in the art. A second sequence, comprising antisense or ribozymes against the rape cDNA (Example 5) can be introduced for simultaneous expression. The resultant transformed plant is expected to have 2-AT activity corresponding to that of *L. douglassii*, with concurrent down regulation of the native rape 2-AT gene.

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The modified OSR plant thus obtained had higher levels of erucic acid in position 2 of its triacylglycerols than wild type plants. In addition higher levels of trierucin are found in the seed oil.

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EXAMPLE 9

Genomic library screening

The sequence given in Figure 1 is used to screen a genomic library of *Arabidopsis* and a hybrid using clone 10 obtained. Using standard techniques, a promoter may be derived from this clone. The promoter may be used to drive expression in plant cell membranes.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES

(iii) NUMBER OF SEQUENCES: 7

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: WO PCT/GB93/_____

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1514 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 130..1254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCCCGTCCCTC CTCGTCGCCG GCGGAGCCGC CTACTATCGC CTGGAGAAAGG AGGCCCGCGG	60
GGAGCTTTTC CCACTGCCGA CTGCCGTCTG ACCCTCCGAG ATCGGAAGCG GCGCCGGCGC	120
CGGCCGGCG ATG GCG ATC CCG CTC GTG CTC GTC GTG CTC CCG CTC GGC	168
Met Ala Ile Pro Leu Val Leu Val Val Leu Pro Leu Gly	

CTG CTC TTC CTC CTG TCC GCC CTC ATC GTC AAC GCC ATC CAG GCC GTC Leu Leu Phe Leu Leu Ser Gly Leu Ile Val Asn Ala Ile Gln Ala Val 15 20 25	216
CTA TTT GTG ACG ATA AGG CCC TTT TCG AAG AGC TTC TAC CGT CGG ATC Leu Phe Val Thr Ile Arg Pro Phe Ser Lys Ser Phe Tyr Arg Arg Ile 30 35 40 45	264
AAC AGA TTC TTG GCC GAG CTG CTG TGG CTT CAG CTT GTC TGG GTG GTG Asn Arg Phe Leu Ala Glu Leu Leu Trp Leu Gln Leu Val Trp Val Val 50 55 60	312
GAC TGG TGG GCA GGT GTT AAG GTA CAA CTG CAT GCA GAT GAG GAA ACT Asp Trp Trp Ala Gly Val Lys Val Gln Leu His Ala Asp Glu Glu Thr 65 70 75	360
TAC AGA TCA ATG GGT AAA GAG CAT GCA CTC ATC ATA TCA AAT CAT CGG Tyr Arg Ser Met Gly Lys Glu His Ala Leu Ile Ile Ser Asn His Arg 80 85 90	408
AGT GAT ATT GAT TGG CTC ATT GGA TGG ATA TTG GCC CAG CGT TCA GGG Ser Asp Ile Asp Trp Leu Ile Gly Trp Ile Leu Ala Gln Arg Ser Gly 95 100 105	456
TGC CTT GGA AGT ACA CTT GCT GTC ATG AAG AAG TCA TCC AAG TTC CTT Cys Leu Gly Ser Thr Leu Ala Val Met Lys Lys Ser Ser Lys Phe Leu 110 115 120 125	504
CCA GTT ATT GGC TGG TCA ATG TGG TTT GCA GAG TAC CTC TCT TTG GAA Pro Val Ile Gly Trp Ser Met Trp Phe Ala Glu Tyr Leu Phe Leu Glu 130 135 140	552
AGG AGC TGG GCC AAG GAT GAA AAG ACA CTA AAG TGG GGT CTC CAA AGG Arg Ser Trp Ala Lys Asp Glu Lys Thr Leu Lys Trp Gly Leu Gln Arg 145 150 155	600
TTG AAA GAC TTC CCT AGA CCA TTT TGG CTA GCT CTT TTC GTC GAG GGT Leu Lys Asp Phe Pro Arg Pro Phe Trp Leu Ala Leu Phe Val Glu Gly 160 165 170	648
ACT CGC TTT ACT CCA GCA AAG CTT CTC GCA GCT CAG GAA TAT GCG GCC Thr Arg Phe Thr Pro Ala Lys Leu Leu Ala Ala Gln Glu Tyr Ala Ala 175 180 185	696
TCC CAG GGC TTA CCG GCT CCT AGA AAT GTA CTT ATT CCA CGT ACC AAG Ser Gln Gly Leu Pro Ala Pro Arg Asn Val Leu Ile Pro Arg Thr Lys 190 195 200 205	744
GGA TTT GTA TCT GCT GTA AGT ATT ATG CGA GAT TTT GTT CCA GCC ATT Gly Phe Val Ser Ala Val Ser Ile Met Arg Asp Phe Val Pro Ala Ile 210 215 220	792
TAT GAT ACA ACT GTA ATA GTC CCT AAA GAT TCC CCT CAA CCA ACA ATG Tyr Asp Thr Thr Val Ile Val Pro Lys Asp Ser Pro Gln Pro Thr Met 225 230 235	840
CTG CGG ATT TTG AAA GGG CAA TCA TCA GTG ATA CAT GTC CGC ATG AAA Leu Arg Ile Leu Lys Gly Gln Ser Ser Val Ile His Val Arg Met Lys 240 245 250	888
CGT CAT GCA ATG AGT GAG ATG CCA AAA TCA GAT GAG GAT GTT TCA AAA Arg His Ala Met Ser Glu Met Pro Lys Ser Asp Glu Asp Val Ser Lys 255 260 265	936

TGG TGT AAA GAC ATT TTT GTG GCA AAG GAT GCC TTA CTG GAC AAG CAT Trp Cys Lys Asp Ile Phe Val Ala Lys Asp Ala Leu Leu Asp Lys His 270 275 280 285	984
TTG GCA ACA GGC ACT TTC GAT GAG GAG ATT AGA CCT ATT GGC CGT CCA Leu Ala Thr Gly Thr Phe Asp Glu Glu Ile Arg Pro Ile Gly Arg Pro 290 295 300	1032
GTG AAA TCA TTG CTG GTG ACC CTG TTC TGG TCG TGC CTC CTG CTG TTT Val Lys Ser Leu Leu Val Thr Leu Phe Trp Ser Cys Leu Leu Leu Phe 305 310 315	1080
GGC GCC ATC GAG TTC TTC AAG TGG ACA CAG CTT CTG TCG ACG TGG AGG Gly Ala Ile Glu Phe Phe Lys Trp Thr Gln Leu Leu Ser Thr Trp Arg 320 325 330	1128
GGT GTG GCG TTC ACT GCC GCA GGG ATG GCG CTT GTG ACG GGT GTC ATG Gly Val Ala Phe Thr Ala Ala Gly Met Ala Leu Val Thr Gly Val Met 335 340 345	1176
CAT GTC TTC ATC ATG TTC TCC CAG GCT GAG CGG TCG AGC TCA GCC AGG His Val Phe Ile Met Phe Ser Gln Ala Glu Arg Ser Ser Ser Ala Arg 350 355 360 365	1224
GCG GCA CGG AAC CGG GTC AAG AAG GAA TGAAAAATGG AGGGTGAGA Ala Ala Arg Asn Arg Val Lys Lys Glu 370 375	1271
TGAGGTTCTC GTGGGGTTTG TTATGGCAA CCTTCAAAAG GACTCTCCAT TCATATTAGT ATTAATTCTAT ATATATGCAG CGCCAAATTC CAGACATTGA TATGCTCTCA AATAGGATGT TCTGCTCCCC TCTTGTATTT GTATGCAGGA AAGGGTTTGT AGGGAGTTA CCCCCCCCCC CCCCCCCCCCC GCCTTTCTTT GGGGAAGAAA GACATATTCT GGAAGCCTTC CAGTAGTTCA	1331 1391 1451 1511
AAA	1514

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Ile Pro Leu Val Leu Val Val Leu Pro Leu Gly Leu Leu Phe
1 5 10 15

Leu Leu Ser Gly Leu Ile Val Asn Ala Ile Gln Ala Val Leu Phe Val
20 25 30

Thr Ile Arg Pro Phe Ser Lys Ser Phe Tyr Arg Arg Ile Asn Arg Phe
35 40 45

Leu Ala Glu Leu Leu Trp Leu Gln Leu Val Trp Val Val Asp Trp Trp
50 55 60

Ala Gly Val Lys Val Gln Leu His Ala Asp Glu Glu Thr Tyr Arg Ser
65 70 75 80

Met Gly Lys Glu His Ala Leu Ile Ile Ser Asn His Arg Ser Asp Ile
85 90 95

Asp Trp Leu Ile Gly Trp Ile Leu Ala Gln Arg Ser Gly Cys Leu Gly
100 105 110

Ser Thr Leu Ala Val Met Lys Lys Ser Ser Lys Phe Leu Pro Val Ile
115 120 125

Gly Trp Ser Met Trp Phe Ala Glu Tyr Leu Phe Leu Glu Arg Ser Trp
130 135 140

Ala Lys Asp Glu Lys Thr Leu Lys Trp Gly Leu Gln Arg Leu Lys Asp
145 150 155 160

Phe Pro Arg Pro Phe Trp Leu Ala Leu Phe Val Glu Gly Thr Arg Phe
165 170 175

Thr Pro Ala Lys Leu Leu Ala Ala Gln Glu Tyr Ala Ala Ser Gln Gly
180 185 190

Leu Pro Ala Pro Arg Asn Val Leu Ile Pro Arg Thr Lys Gly Phe Val
195 200 205

Ser Ala Val Ser Ile Met Arg Asp Phe Val Pro Ala Ile Tyr Asp Thr
210 215 220

Thr Val Ile Val Pro Lys Asp Ser Pro Gln Pro Thr Met Leu Arg Ile
225 230 235 240

Leu Lys Gly Gln Ser Ser Val Ile His Val Arg Met Lys Arg His Ala
245 250 255

Met Ser Glu Met Pro Lys Ser Asp Glu Asp Val Ser Lys Trp Cys Lys
260 265 270

Asp Ile Phe Val Ala Lys Asp Ala Leu Leu Asp Lys His Leu Ala Thr
275 280 285

23

Gly Thr Phe Asp Glu Glu Ile Arg Pro Ile Gly Arg Pro Val Lys Ser
290 295 300

Leu Leu Val Thr Leu Phe Trp Ser Cys Leu Leu Leu Phe Gly Ala Ile
305 310 315 320

Glu Phe Phe Lys Trp Thr Gln Leu Leu Ser Thr Trp Arg Gly Val Ala
325 330 335

Phe Thr Ala Ala Gly Met Ala Leu Val Thr Gly Val Met His Val Phe
340 345 350

Ile Met Phe Ser Gln Ala Glu Arg Ser Ser Ser Ala Arg Ala Ala Arg
355 360 365

Asn Arg Val Lys Lys Glu
370

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Tyr Phe Val Glu Gly Gly Arg Ser Arg Thr Gly Arg Leu Leu Asp
1 5 10 15

25

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Phe Pro Glu Gly Thr Arg Ser Arg Gly Arg Gly Leu Leu Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Leu Phe Val Glu Gly Thr Arg Phe Thr Pro Ala Lys Leu Leu Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ala Ile Pro Leu Val Leu Val Val Leu Pro Leu Gly Leu Leu Phe
1 5 10 15

Leu Leu Ser Gly Leu Ile Val Asn Ala Ile Gln Ala Val Leu Phe Val
20 25 30

Thr Ile Arg Pro Phe Ser Lys Ser Phe Tyr Arg Arg Ile Asn Arg Phe
35 40 45

Leu Ala Glu Leu Leu Trp Leu Gln Leu Val Trp Val Val Asp Trp Trp
50 55 60

Ala Gly Val Lys Val Gln Leu His Ala Asp Glu Glu Thr Tyr Arg Ser
65 70 75 80

Met Gly Lys Glu His Ala Leu Ile Ile Ser Asn His Arg Ser Asp Ile
85 90 95

Asp Trp Leu Ile Gly Trp Ile Leu Ala Gln Arg Ser Gly Cys Leu Gly
100 105 110

Ser Thr Leu Ala Val Met Lys Lys Ser Ser Lys Phe Leu Pro Val Ile
115 120 125

Gly Trp Ser Met Trp Phe Ala Glu Tyr Leu Phe Leu Glu Arg Ser Trp
130 135 140

Ala Lys Asp Glu Lys Thr Leu Lys Trp Gly Leu Gln Arg Leu Lys Asp
145 150 155 160

Phe Pro Arg Pro Phe Trp Leu Ala Leu Phe Val Glu Gly Thr Arg Phe
165 170 175

Thr Pro Ala Lys Leu Leu Ala Ala Gln Glu Tyr Ala Ala Ser Gln Gly
180 185 190

Leu Pro Ala Pro Arg Asn Val Leu Ile Pro Arg Thr Lys Gly Phe Val
195 200 205

Ser Ala Val Ser Ile Met Arg Asp Phe Val Pro Ala Ile Tyr Asp Thr
210 215 220

Thr Val Ile Val Pro Lys Asp Ser Pro Gln Pro Thr Met Leu Arg Ile
225 230 235 240

Leu Lys Gly Gln Ser Ser Val Ile His Val Arg Met Lys Arg His Ala
245 250 255

Met Ser Glu Met Pro Lys Ser Asp Glu Asp Val Ser Lys Trp Cys Lys
260 265 270

Asp Ile Phe Val Ala Lys Asp Ala Leu Leu Asp Lys His Leu Ala Thr
275 280 285

Gly Thr Phe Asp Glu Glu Ile Arg Pro Ile Gly Arg Pro Val Lys Ser
290 295 300

Leu Leu Val Thr Leu Phe Trp Ser Cys Leu Leu Leu Phe Gly Ala Ile
305 310 315 320

Glu Phe Phe Lys Trp Thr Gln Leu Leu Ser Thr Trp Arg Gly Val Ala
325 330 335

Phe Thr Ala Ala Gly Met Ala Leu Val Thr Gly Val Met His Val Phe
340 345 350

Ile Met Phe Ser Gln Ala Glu Arg Ser Ser Ser Ala Arg Ala Ala Arg
355 360 365

Asn Arg Val Lys Lys Glu
370

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 295 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Ala Met Ala Ala Ala Val Ile Val Pro Leu Gly Ile Leu Phe Phe
 1 5 10 15

Ile Ser Gly Leu Val Val Asn Leu Leu Gln Arg Ser Gly Cys Leu Gly
 20 25 30

Ser Ala Leu Ala Val Met Lys Lys Ser Ser Lys Phe Leu Pro Val Ile
 35 40 45

Gly Trp Ser Met Trp Phe Ser Glu Tyr Leu Phe Leu Glu Arg Asn Trp
 50 55 60

Ala Lys Asp Glu Ser Thr Leu Lys Ser Gly Leu Gln Arg Leu Asn Asp
 65 70 75 80

Phe Pro Arg Pro Phe Trp Leu Ala Leu Phe Val Glu Gly Thr Arg Phe
 85 90 95

Thr Glu Ala Lys Leu Lys Ala Ala Gln Glu Tyr Ala Ala Ser Ser Glu
 100 105 110

Leu Pro Val Pro Arg Asn Val Leu Ile Pro Arg Thr Lys Gly Phe Val
 115 120 125

Ser Ala Val Ser Asn Met Arg Ser Phe Val Pro Ala Ile Tyr Asp Met
 130 135 140

Thr Val Ala Ile Pro Lys Thr Ser Pro Pro Pro Thr Met Leu Arg Leu
 145 150 155 160

Phe Lys Gly Gln Pro Ser Val Val His Val His Ile Lys Cys His Ser
 165 170 175

Met Lys Asp Leu Pro Glu Ser Glu Asp Glu Ile Ala Gln Trp Cys Arg
 180 185 190

Asp Gln Phe Val Thr Lys Asp Ala Leu Leu Asp Lys His Ile Ala Ala
 195 200 205

Asp Thr Phe Ala Gly Gln Lys Glu Gln Asn Ile Gly Arg Pro Ile Lys
 210 215 220

Ser Leu Ala Val Val Leu Ser Trp Ala Cys Leu Leu Thr Leu Gly Ala
 225 230 235 240

Met Lys Phe Leu His Trp Ser Asn Leu Phe Ser Ser Trp Lys Gly Ile
 245 250 255

Ala Leu Ser Ala Leu Gly Leu Gly Ile Ile Thr Leu Cys Met Gln Ile
 260 265 270

Leu Ile Arg Ser Ser Gln Ser Glu Arg Ser Thr Pro Ala Lys Val Ala
 275 280 285

29

Pro Ala Lys Pro Lys Asp Asn
290 295

CLAIMS

1. A recombinant or isolated DNA sequence selected from
 - 5 (i) a DNA sequence comprising the DNA sequence of Figure 1 encoding at least from Met₄₄ to Stop₄₁₈ (SEQ ID: 2) or its complementary strand;
 - 10 (ii) nucleic acid sequences hybridising to the DNA sequence of Figure 1 (SEQ ID: 1) or its complementary strand under stringent conditions; and
 - 15 (iii) nucleic acid sequences which would hybridise to the DNA sequence of Figure 1 (SEQ ID: 1), or its complementary strand, but for the degeneracy of the genetic code.
2. A DNA sequence as claimed in claim 1 which encodes an enzyme having membrane-bound acyltransferase activity.
3. A DNA sequence as claimed in claim 2, in which the acyltransferase activity is 2-acyltransferase activity.
- 25 4. An isolated protein which is the expression product of a DNA sequence as claimed in claim 1, 2 or 3.
5. An antibody capable of specifically binding to a protein as claimed in claim 4.
- 30 6. A plant having one or more insoluble acyltransferase enzymes having a substrate specificity which differs from the native enzyme of the plant.

7. A plant as claimed in claim 6, which is transgenic for an insoluble acyltransferase enzyme from another species.

5 8. A plant as claimed in claim 6 or 7, which is rape, maize, sunflower or soya.

10 9. A plant as claimed in claim 7, wherein the said other species is a species of the genus *Limnanthes* (such as *L. alba* or, preferably, *L. douglassii*) or *Crambe*.

15 10. A plant as claimed in any one of claims 6 to 9, wherein the insoluble acyltransferase enzyme is 2-acyltransferase.

11. A plant as claimed in claim 10, wherein the 2-acyltransferase has a higher specificity for erucic acid than the native enzyme of the plant.

20 12. A plant as claimed in any one of claims 6 to 11, wherein the said native enzyme is at least partially rendered inoperative or removed, for example by a ribozyme or by antisense nucleic acid.

25 13. A method of generating oil, the method comprising cultivating a plant as claimed in anyone of claims 6 to 12 and harvesting oil produced by the plant or a part (particularly seeds) thereof.

30 14. A microbial host capable of expressing a DNA sequence as claimed in claim 1, 2 or 3.

15. A protein which is substantially homologous to a protein as claimed in claim 4.

16. A fragment of a DNA sequence as claimed in claim 1, 2 or 3, comprising at least 15 nucleotides.
5. 17. DNA encoding RNA which is antisense to RNA encoded by DNA as claimed in claim 1, 2 or 3.
18. DNA encoding a ribozyme specific to RNA encoded by DNA as claimed in claim 1, 2 or 3.
10. 19. Isolated or recombinant DNA containing a promoter which naturally drives expression of a gene to produce a protein as claimed in claim 4 or 15.

1 / 8

FIG. 1 (1/3)

1/1	CCC	CGT	CCT	CCT	CGT	CGC	CGG	CGG	AGC	CGC	CGG	CGG	GAA	GGA	GCG	CCG	CGG	
P R	P P	R R	R R	R R	S R	S R	R S	R S	T L	C T	L L	L L	S P	P G	E G	A P	R	
61/21	GGA	GCT	TTT	CCC	ACT	GCC	GAC	TGC	CGT	CTG	ACC	CTC	CGA	GAT	CGG	AAG	CGG	CGC
G A	F P	P T	A D	C D	R L	T L	R L	T L	R L	T L	R D	R K	R R	R R	R R	R R	R R	
121/41	CGG	CCG	GCG	ATG	GCG	ATC	CCG	CTC	GTG	CTG	GTC	GRG	CTC	CCG	CTG	CTG	CTC	CTC
R P	A M	A I	P L	V L	V L	V L	V L	V L	V L	P L	P L	P L	G L	L F	L F	L	L	
181/61	CTG	TCC	GGC	CTC	ATC	GTC	AAC	GCC	ATC	CAG	GCC	GTC	CTA	TTT	GTG	ACG	ATA	AGG
L S	G L	I I	V N	A I	Q A	Q I	A V	A V	L F	V T	V T	V T	I R	P P	F F			
241/81	TCG	AAG	AGC	TTC	TAC	CGT	CGG	ATC	AAC	AGA	TTC	TTG	GCC	GAG	CTG	CTG	CTT	CAG
S K	S F	F Y	R R	I I	N N	R R	F L	A A	E L	L L	W W	W W	L Q	L Q	L Q	L Q	L Q	
301/101	GTC	TGG	GTG	GAC	TGG	TGG	GCA	GCA	GTT	AAG	GTA	CAA	CTG	CAT	GCA	GAT	GAG	GAA
V W	V V	D W	W W	A G	V V	K V	Q L	V K	V K	V K	H A	D E	E T					
361/121	TAC	AGA	TCA	ATG	GGT	AAA	GAG	CAT	GCA	CTC	ATC	ATA	TCA	AAT	CAT	CGG	AGT	GAT
Y R	S M	G G	K K	E H	H A	L I	I I	S N	H R	S D	D I	D V						
421/141	TGG	CTC	ATT	GGA	TGG	ATA	TGG	GCC	CAG	CGT	TCA	GGG	TGC	CTT	GGA	AGT	ACA	CTT
W L	I I	G W	W I	L A	Q R	S G	C L	G S	T L	A V								
481/161	ATG	AAG	TCA	TCC	AAG	TTC	CTT	CCA	GTT	ATT	GGC	TGG	TCA	ATG	TGG	TTT	GCA	GAG
M K	K S	S S	K R	F F	L P	V I	G W	S M	W F	A E	Y							
541/181	CTC	TTG	GAA	AGG	AGC	TGG	GCC	AAG	GAT	GAA	AAG	ACA	CTA	AAG	TGG	GGT	CTC	CAA
L F	L E	E R	S W	A K	D E	K T	L K	W G	L Q	W G	L Q	R R						

2 / 8
FIG.1

601/201	TTG AAA GAC TTC CCT AGA CCA TTT TGG CTA GCT CTT TTC GTC GAG GGT ACT CGC CCT ACT	
L K D F P R P F W L A L F V E G T R F T	691/231	
661/221	CCA GCA AAG CTT CTC GCA GCT CAG GAA TAT GCG GCG TCC CAG GGC TTA CCG GCT CCT AGA	
P A K L A A Q E Y A A S Q G L P A P R	721/241	
N V L I P R T K G F V S A V S I M R D F	811/271	
841/281	ATT GTA CTT ATT CCA CGT ACC AAG GGA TTT GTA TCT GCT GTA AGT ATT ATG CGA GAT TTT	
V P A I Y D T T V I V P K D S P Q T M	871/291	
L R I L K G Q S S V I H V R M K R H A M	901/301	
S E M P K S D E D V S K W C K D I F V A	991/331	
961/321	AGT GAG ATG CCA AAA TCA GAT GAG GAT GTT TCA AAA TGG TGT AAA GAC ATT TTT GTG GCA	
K D A L L D K H L A T G T F D E I R P	1021/341	
I G R P V K S L L V T L F W S C L L F	1081/361	
G A I E F F K W T Q L S T W R G V A F	1111/371	
SUBSTITUTE SHEET	1051/351	
ATT GGC CGT CCA GTG AAA TCA TTG CTG GTG ACC CTG TTC TGG TCG TGC CTC CTG CTG TTT		

3 / 8

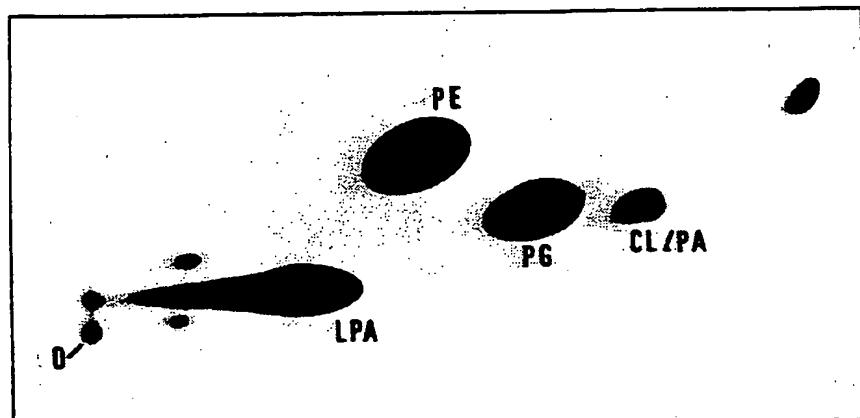
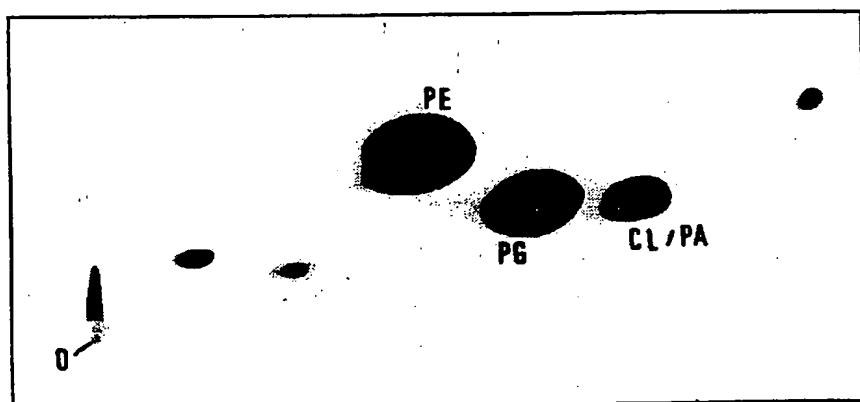
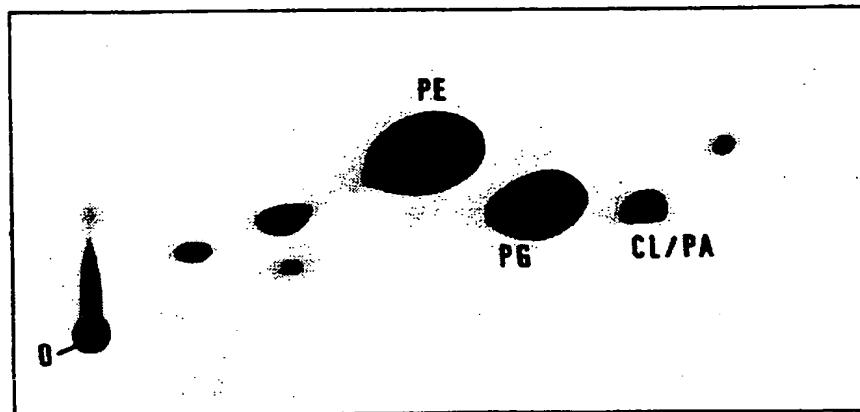
1141/381	ACT GCC GCA GGG ATG GCG CTT GTG ACG GGT GTC ATG CAT GTC TTC ATC ATG TTC TCC CAG	1171/391	T A G M A L V T G V M H V F I M F S Q
T A	A G M A L V T G V M H V F I M F S Q	1201/401	1231/411
1201/401	GCT GAG CGG TCG AGC TCA GCC AGG GCG GCA CGG AAC CGG GTC AAG AAG GAA TGA AAA ATG	A E R S S A R A A R N R V K K E * K M	
A E R S S A R A A R N R V K K E * K M	1261/421	1291/431	
1261/421	GAG GGT GGA GAT GAG GTT CTC GTG GGG TTT GTT ATG GGC AAC CTT CAA AAG GAC TCT CCA	E G D E V L V G F V M G N L Q K D S P	
E G D E V L V G F V M G N L Q K D S P	1321/441	1351/451	
1321/441	TTC ATA TTA GTA TTA ATT CAT ATA TAT GCA GCG CCA AAT TCC AGA CAT TGA TAT GCT CTC	F I L V L I H I Y A A P N S . R H * Y A L	
F I L V L I H I Y A A P N S . R H * Y A L	1381/461	1411/471	
1381/461	AAA TAG GAT GTT CTG CTC CCC TCT TGT ATT TGT ATG CAG GAA AGG GTT TGT AGG GAG TTT	K * D V L L P S C I C M Q E R V C R E F	
K * D V L L P S C I C M Q E R V C R E F	1441/481	1471/491	
1441/481	ACC CCC CCC CCC CCC CCC GCC TTT CTT TGG Gga AGA AAG ACA Tat TCT GGA AGC CTT	T P P P A F L W G R K T Y S G S L	
T P P P A F L W G R K T Y S G S L	1501/501		
1501/501	CCA GTA GTT CAA AA	P V V Q	

FIG. 1 (3/3)

4 / 8

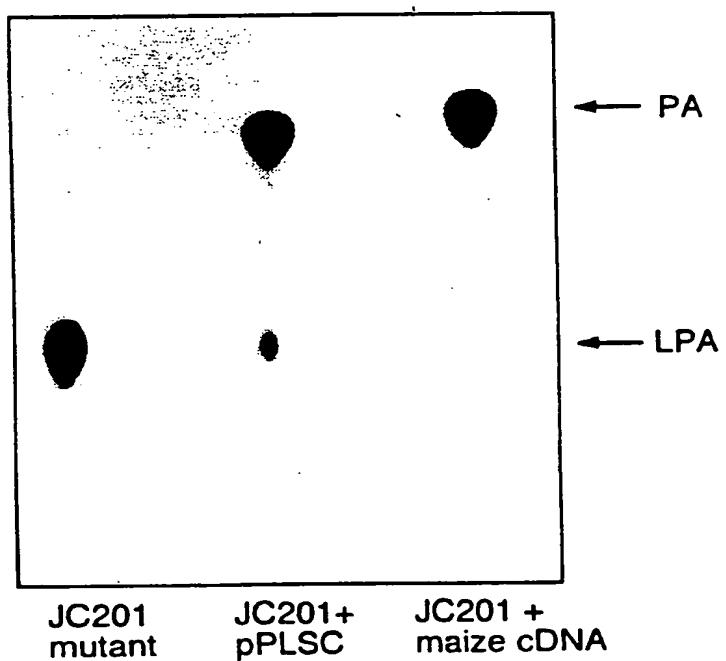
FIG. 2

plsB	-	Y	F	V	E	G	G	R	S	R	T	G	R	L	L	L	D	-
plsC	-	M	F	P	E	G	T	R	S	R	G	R	G	L	L	P	-	
maize	-	L	F	V	E	G	T	R	F	T	P	A	K	L	L	A	-	
		*	+	*	*	+	*	+	*	+	+	*	*	*	*	*	*	

5 / 8
FIG. 3A : mutant
JC201B : mutant +
pPLSCC : mutant +
maize
cDNA

6 / 8

FIG. 4



SUBSTITUTE SHEET

7 / 8

FIG. 5 (1/2)

Maize = 374 aa vs. rape = 311 aa

51.5% identity; Optimized score: 705

	10	20	30	40	50	60
maize	MAIPLVVLVVIPPLGLLIFLLSGLIVNAIQAVLFVTIRPFSKSFYRRRINRFLAELLWFLQLVWV					
rape	MAAAVIVPLGILFFISGLVVN-----					
	70	80	90	100	110	120
maize	VDWWAGVKVQVLHADETYRSMGREHALIIISNHRSDIDWLIGWILIAQRSGCLGSTLAVMKK					
rape	-----					
	130	140	150	160	170	180
maize	SSKFLPVIGWSMMFAEYLFLERSWAKEDEKTLKWGLQRLKDFPRPFWLALFVEGTRFTPAK					
rape	SSKFLPVIGWSMMWFSEYFLERNWAKEDESTLKSGLQRLNDDFPRPFWLALFVEGTRFTPEAK	50	60	70	80	90
	100	100	100	100	100	100

				8 / 8
maize	LLAAQEYAASQGLPAPRNVLIPRTKGFVSAVSIMRDFVPAIYDRTVIVPKDSPQPTMLRI	190	200	210 220 230 240
rape	LKAAQEYAASSELPPVPRNVLIPRTKGFVSAVNMRSFVPAIYDMTVAIPKTSPPPTMLRL	110	120	130 140 150 160
maize	LKGQSSVIHVTRMRRHAMSEMPKSDEDVSKWCKDIFTVAKDALLDKHLATGTF-DEEIRPIG	250	260	270 280 290
rape	FRGQPSVTVHVKCHSMKDLPESEDEIAQWCRDQFVTKDHALLDKHIADTFAGQKEQNIG	170	180	190 200 210 220
maize	RPVKSLLVTLFWSCLLFGAIEFFKWTQLLISTWRGVFTAAGMALVTVGMHVFIMFSQAE	300	310	320 330 340 350
rape	RPIKSLAVVLSWACLLTGAMKFLHWSNLFSSWKGIALSALGLGITLCMQILIRSSQSE	230	240	250 260 270 280
maize	RSSSARAARNRVKKE	360	370	380
rape	RSTPAKVAPAKPKDN	290		

FIG. 5 (2/2)

INTERNATIONAL SEARCH REPORT

Internal Application No
PCT/GB 93/02528

A. CLASSIFICATION OF SUBJECT MATTER
 IPC 5 C12N15/54 C12N15/82 C12N15/11 C12N9/10 A01H5/00
 C11B1/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
 IPC 5 C12N A01H C11B

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
O, X	FAT SCIENCE TECHNOLOGY. 47TH ANNUAL MEETING OF THE GERMAN SOCIETY FOR FAT SCIENCE, 2-5 SEPTEMBER, 1991. vol. 93, no. 11, November 1991 pages 417 - 418 PETEREK, G., ET AL. 'Wege zur Klonierung der 1-Acylglycerin-3-Phosphat-Acyltransferase' see the whole document	1-4, 14, 15
Y	---	6-13, 16, 17

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

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Date of the actual completion of the international search

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INTERNATIONAL SEARCH REPORT

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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A	<p>PLANT PHYSIOLOGY vol. 91 , 1989 pages 1288 - 1295 OO, K-C, ET AL. 'Lysophosphatidate acyltransferase activities in the microsomes from palm endosperm, maize scutellum, and rapeseed cotyledon of maturing seeds' see the whole document -----</p>	5

INTERNATIONAL SEARCH REPORT

Information on patent family members

Intern. Application No

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